

PL #10



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,571

DATE: 10/16/2003
TIME: 11:20:06

Input Set : A:\PA90631US.ST25.txt
Output Set: N:\CRF4\10162003\J009571.raw

ENTERED

3 <110> APPLICANT: Dear, Neil T.
 5 <120> TITLE OF INVENTION: NOVEL CALPAINS AND THE USE THEREOF
 7 <130> FILE REFERENCE: PA90631US-01938/GRI
 9 <140> CURRENT APPLICATION NUMBER: US 10/009,571
 C--> 10 <141> CURRENT FILING DATE: 2003-03-17
 12 <150> PRIOR APPLICATION NUMBER: DE 19928021.5
 13 <151> PRIOR FILING DATE: 1999-06-18
 15 <160> NUMBER OF SEQ ID NOS: 2
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2338
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: 5'UTR
 26 <222> LOCATION: (1)..(103)
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (104)..(2212)
 32 <220> FEATURE:
 33 <221> NAME/KEY: 3'UTR
 34 <222> LOCATION: (2213)..(2338)
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 37 ctccccaggg ccgagtccttc cggagtcagc agagagcctg gatggatcac aggaggataa 60
 39 gcctcggggc tcatgtgcgg agcccacttt tactgataacg gga atg gtg gct cac 115
 40 Met Val Ala His
 41 1
 43 ata aac aac agc cgg ctc aag gcc aag ggc gtg ggc cag cac gac aac 163
 44 Ile Asn Asn Ser Arg Leu Lys Ala Lys Gly Val Gly Gln His Asp Asn
 45 5 10 15 20
 47 gcc cag aac ttt ggt aac cag agc ttt gag gag ctg cga gca gcc tgt 211
 48 Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu Arg Ala Ala Cys
 49 25 30 35
 51 cta aga aag ggg gag ctc ttc gag gac ccc tta ttc cct gct gaa ccc 259
 52 Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe Pro Ala Glu Pro
 53 40 45 50
 55 agc tca ctg ggc ttc aag gac ctg ggc ccc aac tcc aaa aat gtg cag 307
 56 Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser Lys Asn Val Gln
 57 55 60 65
 59 aac atc tcc tgg cag cgg ccc aag gat atc ata aac aac cct cta ttc 355
 60 Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn Asn Pro Leu Phe
 61 70 75 80
 63 atc atg gat ggg att tct cca aca gac atc tgc cag ggg atc ctc ggg 403

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64	Ile	Met	Asp	Gly	Ile	Ser	Pro	Thr	Asp	Ile	Cys	Gln	Gly	Ile	Leu	Gly	
65	85				90					95				100			
67	gac	tgc	tgg	ctg	ctg	gct	gcc	atc	ggc	tcc	ctt	acc	acc	tgc	ccc	aaa	451
68	Asp	Cys	Trp	Leu	Leu	Ala	Ala	Ile	Gly	Ser	Leu	Thr	Thr	Cys	Pro	Lys	
69					105					110				115			
71	ctg	cta	tac	cgc	gtg	gtg	ccc	aga	gga	cag	agc	ttc	aag	aaa	aac	tat	499
72	Leu	Leu	Tyr	Arg	Val	Val	Pro	Arg	Gly	Gln	Ser	Phe	Lys	Lys	Asn	Tyr	
73					120					125				130			
75	gct	ggc	atc	ttc	cat	ttt	cag	att	tgg	cag	ttt	gga	cag	tgg	gtg	aac	547
76	Ala	Gly	Ile	Phe	His	Phe	Gln	Ile	Trp	Gln	Phe	Gly	Gln	Trp	Val	Asn	
77					135					140				145			
79	gtg	gtg	gta	gat	gac	cg	ctg	ccc	aca	aag	aat	gac	aag	ctg	gtg	ttt	595
80	Val	Val	Val	Asp	Asp	Arg	Leu	Pro	Thr	Lys	Asn	Asp	Lys	Leu	Val	Phe	
81					150					155				160			
83	gtg	cac	tca	acc	gaa	cgc	agt	gag	ttc	tgg	agt	gcc	ctg	ctg	gag	aag	643
84	Val	His	Ser	Thr	Glu	Arg	Ser	Glu	Phe	Trp	Ser	Ala	Leu	Leu	Glu	Lys	
85					165					170				175			180
87	gcg	tat	gcc	aag	ctg	agt	ggg	tcc	tat	gaa	gca	ttg	tca	ggg	ggc	agt	691
88	Ala	Tyr	Ala	Lys	Leu	Ser	Gly	Ser	Tyr	Glu	Ala	Leu	Ser	Gly	Gly	Ser	
89					185					190				195			
91	acc	atg	gag	ggc	ttt	gag	gac	ttc	aca	gga	ggc	gtg	gcc	cag	agc	ttc	739
92	Thr	Met	Glu	Gly	Leu	Glu	Asp	Phe	Thr	Gly	Gly	Val	Ala	Gln	Ser	Phe	
93					200					205				210			
95	caa	ctc	cag	agg	ccc	cct	cag	aac	ctg	ctc	agg	ctc	ctt	agg	aag	gcc	787
96	Gln	Leu	Gln	Arg	Pro	Pro	Gln	Asn	Leu	Leu	Arg	Leu	Leu	Arg	Lys	Ala	
97					215					220				225			
99	gtg	gag	cga	tcc	tcc	ctc	atg	ggt	tgc	tcc	att	gaa	gtc	acc	agt	gat	835
100	Val	Glu	Arg	Ser	Ser	Leu	Met	Gly	Cys	Ser	Ile	Glu	Val	Thr	Ser	Asp	
101					230					235				240			
103	agt	gaa	ctg	gaa	tcc	atg	act	gac	aag	atg	ctg	gtg	aga	ggg	cac	gct	883
104	Ser	Glu	Leu	Glu	Ser	Met	Thr	Asp	Lys	Met	Leu	Val	Arg	Gly	His	Ala	
105					245					250				255			260
107	tac	tct	gtg	act	ggc	ttt	cag	gat	gtc	cac	tac	aga	ggc	aaa	atg	gaa	931
108	Tyr	Ser	Val	Thr	Gly	Leu	Gln	Asp	Val	His	Tyr	Arg	Gly	Lys	Met	Glu	
109					265					270				275			
111	aca	ctg	att	cgg	gtc	cg	aat	ccc	tgg	ggc	cg	att	gag	tgg	aat	gga	979
112	Thr	Leu	Ile	Arg	Val	Arg	Asn	Pro	Trp	Gly	Arg	Ile	Glu	Trp	Asn	Gly	
113					280					285				290			
115	gct	tgg	agt	gac	agt	gcc	agg	gag	tgg	gaa	gag	gtg	gcc	tca	gac	atc	1027
116	Ala	Trp	Ser	Asp	Ser	Ala	Arg	Glu	Trp	Glu	Glu	Val	Ala	Ser	Asp	Ile	
117					295					300				305			
119	cag	atg	cag	ctg	ctg	cac	aag	acg	gag	gac	ggg	gag	ttc	tgg	atg	tcc	1075
120	Gln	Met	Gln	Leu	Leu	His	Lys	Thr	Glu	Asp	Gly	Glu	Phe	Trp	Met	Ser	
121					310					315				320			
123	tac	caa	gat	ttc	ctg	aac	aac	ttc	acg	ctc	ctg	gag	atc	tgc	aac	ctc	1123
124	Tyr	Gln	Asp	Phe	Leu	Asn	Asn	Phe	Thr	Leu	Leu	Glu	Ile	Cys	Asn	Leu	
125					325					330				335			340
127	acg	cct	gat	aca	ctc	tct	ggg	gac	tac	aag	acg	tg	cac	acc	acc		1171
128	Thr	Pro	Asp	Thr	Leu	Ser	Gly	Asp	Tyr	Lys	Ser	Tyr	Trp	His	Thr	Thr	

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129	345	350	355	
131	tac gag ggc agc tgg cgc aga ggc agc tcc gca ggg ggc tgc agg			1219
132	Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala Gly Gly Cys Arg			
133	360	365	370	
135	aac cac cct ggc acg ttc tgg acc aac ccc cag ttt aag atc tct ctt			1267
136	Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe Lys Ile Ser Leu			
137	375	380	385	
139	cct gag ggg gat gac cca gag gat gac gca gag ggc aat gtt gtg gtc			1315
140	Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly Asn Val Val Val			
141	390	395	400	
143	tgc acc tgc ctg gtg gcc cta atg cag aag aac tgg cgg cat gca cgg			1363
144	Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp Arg His Ala Arg			
145	405	410	415	420
147	cag cag gga gcc cag ctg cag acc att ggc ttt gtc ctc tac gcg gtc			1411
148	Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val Leu Tyr Ala Val			
149	425	430	435	
151	cca aaa gag ttt cag aac att cag gat gtc cac ttg aag aag gaa ttc			1459
152	Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu Lys Lys Glu Phe			
153	440	445	450	
155	ttc acg aag tat cag gac cac ggc ttc tca gag atc ttc acc aac tca			1507
156	Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile Phe Thr Asn Ser			
157	455	460	465	
159	cgg gag gtg agc agc caa ctc cgg ctg cct ccg ggg gaa tat atc att			1555
160	Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly Glu Tyr Ile Ile			
161	470	475	480	
163	att ccc tcc acc ttt gag cca cac aga gat gct gac ttc ctg ctt cgg			1603
164	Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp Phe Leu Leu Arg			
165	485	490	495	500
167	gtc ttc acc gag aag cac agc gag tca tgg gaa ttg gat gaa gtc aac			1651
168	Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu Asp Glu Val Asn			
169	505	510	515	
171	tat gct gag caa ctc caa gag gaa aag gtc tct gag gat gac atg gac			1699
172	Tyr Ala Glu Gln Leu Gln Glu Lys Val Ser Glu Asp Asp Met Asp			
173	520	525	530	
175	cag gac ttc cta cat ttg ttt aag ata gtg gca gga gag ggc aag gag			1747
176	Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly Glu Gly Lys Glu			
177	535	540	545	
179	ata ggg gtg tat gag ctc cag agg ctg ctc aac agg atg gcc atc aaa			1795
180	Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg Met Ala Ile Lys			
181	550	555	560	
183	ttc aaa agc ttc aag acc aag ggc ttt ggc ctg gat gct tgc cgc tgc			1843
184	Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp Ala Cys Arg Cys			
185	565	570	575	580
187	atg atc aac ctc atg gat aaa gat ggc tct ggc aag ctg ggg ctt cta			1891
188	Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys Leu Gly Leu Leu			
189	585	590	595	
191	gag ttc aag atc ctg tgg aaa aaa ctc aag aaa tgg atg gac atc ttc			1939
192	Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp Met Asp Ile Phe			
193	600	605	610	

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195 aga gag tgt gac cag gac cat tca ggc acc ttg aac tcc tat gag atg 1987
 196 Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn Ser Tyr Glu Met
 197 615 620 625
 199 cgc ctg gtt att gag aaa gca ggc atc aag ctg aac aac aag gta atg 2035
 200 Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn Asn Lys Val Met
 201 630 635 640
 203 cag gtc ctg gtg gcc agg tat gca gat gat gac ctg atc ata gac ttt 2083
 204 Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Asp Leu Ile Ile Asp Phe
 205 645 650 655 660
 207 gac agc ttc atc agc tgt ttc ctg agg cta aag acc atg ttc aca ttc 2131
 208 Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr Met Phe Thr Phe
 209 665 670 675
 211 ttt cta acc atg gac ccc aag aat act ggc cat att tgc ttg agc ctg 2179
 212 Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile Cys Leu Ser Leu
 213 680 685 690
 215 gaa cag tgg ctg cag atg acc atg tgg gga tag aggcgctgta ggagcctggt 2232
 216 Glu Gln Trp Leu Gln Met Thr Met Trp Gly
 217 695 700
 219 catctctacc agcagcagca gcagcgaggt tctagccag gagggtgggg tgcttcttgt 2292
 221 agccctcagc tctccagtct ctgctgtatga aatggatcc aggtgg 2338
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 225 <211> LENGTH: 702
 226 <212> TYPE: PRT
 227 <213> ORGANISM: Homo sapiens
 229 <400> SEQUENCE: 2
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 233 Gln His Asp Asn Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu
 234 20 25 30
 236 Arg Ala Ala Cys Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe
 237 35 40 45
 239 Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser
 240 50 55 60
 242 Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn
 243 65 70 75 80
 245 Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln
 246 85 90 95
 248 Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr
 249 100 105 110
 251 Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe
 252 115 120 125
 254 Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly
 255 130 135 140
 257 Gln Trp Val Asn Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp
 258 145 150 155 160
 260 Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala
 261 165 170 175
 263 Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu
 264 180 185 190

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266 Ser Gly Gly Ser Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val
 267 195 200 205
 269 Ala Gln Ser Phe Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu
 270 210 215 220
 272 Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu
 273 225 230 235 240
 275 Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val
 276 245 250 255
 278 Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg
 279 260 265 270
 281 Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile
 282 275 280 285
 284 Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val
 285 290 295 300
 287 Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu
 288 305 310 315 320
 290 Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu
 291 325 330 335
 293 Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr
 294 340 345 350
 296 Trp His Thr Thr Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala
 297 355 360 365
 299 Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe
 300 370 375 380
 302 Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly
 303 385 390 395 400
 305 Asn Val Val Val Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp
 306 405 410 415
 308 Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val
 309 420 425 430
 311 Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu
 312 435 440 445
 314 Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile
 315 450 455 460
 317 Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly
 318 465 470 475 480
 320 Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
 321 485 490 495
 323 Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
 324 500 505 510
 326 Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
 327 515 520 525
 329 Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
 330 530 535 540
 332 Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
 333 545 550 555 560
 335 Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
 336 565 570 575
 338 Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys

VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date